

Reminder: Sequence Listing file  
MUST be saved in  
ASCII text format



PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: PCT/US03/27372

DATE: 02/02/2004

TIME: 14:50:43

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\02022004\PU27372.raw

1 <110> APPLICANT: Lauermann, Vit  
3 <120> TITLE OF INVENTION: Targeted release.  
W--> 5 <130> FILE REFERENCE:  
C--> 7 <140> CURRENT APPLICATION NUMBER: PCT/US03/27372  
9 <141> CURRENT FILING DATE: 2003-08-30  
11 <160> NUMBER OF SEQ ID NOS: 111

These are prior data.

Does Not Comply

Corrected Diskette Needed

## ERRORED SEQUENCES

15 <210> SEQ ID NO: 1  
17 <211> LENGTH: 7  
E--> 19 <212> TYPE: peptide  
21 <213> ORGANISM: unknown  
W--> 24 <220> FEATURE:  
W--> 24 <223> OTHER INFORMATION:  
W--> 24 <400> 1  
26 SMSIARL  
30 <210> SEQ ID NO: 2  
32 <211> LENGTH: 13  
E--> 34 <212> TYPE: peptide  
36 <213> ORGANISM: unknown  
W--> 39 <220> FEATURE:  
W--> 39 <223> OTHER INFORMATION:  
W--> 39 <400> 2  
41 SKGSFSIQYT YHV  
45 <210> SEQ ID NO: 3  
47 <211> LENGTH: 13  
E--> 49 <212> TYPE: peptide  
51 <213> ORGANISM: unknown  
W--> 54 <220> FEATURE:  
W--> 54 <223> OTHER INFORMATION:  
W--> 54 <400> 3  
56 HLGGSQQLLH' NKQ  
60 <210> SEQ ID NO: 4  
62 <211> LENGTH: 14  
E--> 64 <212> TYPE: peptide  
66 <213> ORGANISM: unknown  
W--> 69 <220> FEATURE:  
W--> 69 <223> OTHER INFORMATION:  
W--> 69 <400> 4  
71 SKGKGTSOY SNT  
75 <210> SEQ ID NO: 5

invalid, per Sequence Rules. Use PRT (This is a global error)  
see p. 5 for error explanation  
DO NOT use one-letter amino acids, per Sequence Rules. Use three-letter amino acids, and number them under every 5 amino acids  
DO NOT use TAB codes between amino acid numbers. Use space characters. Leave one space between each amino acid. See 1.822 of Sequence Rules

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77 <211> LENGTH: 8  
E--> 79 <212> TYPE: peptide  
81 <213> ORGANISM: unknown  
W--> 84 <220> FEATURE:  
W--> 84 <223> OTHER INFORMATION:  
W--> 84 <400> 5  
86 DRVYIHPF -8  
90 <210> SEQ ID NO: 6  
92 <211> LENGTH: 12  
E--> 94 <212> TYPE: peptide  
96 <213> ORGANISM: unknown  
W--> 99 <220> FEATURE:  
W--> 99 <223> OTHER INFORMATION:  
W--> 99 <400> 6  
101 VVCGERGFFY TP -12  
105 <210> SEQ ID NO: 7  
107 <211> LENGTH: 7  
E--> 109 <212> TYPE: peptide  
111 <213> ORGANISM: unknown  
W--> 114 <220> FEATURE:  
W--> 114 <223> OTHER INFORMATION:  
W--> 114 <400> 7  
116 FFYTPKA -7  
120 <210> SEQ ID NO: 8  
122 <211> LENGTH: 9  
E--> 124 <212> TYPE: peptide  
126 <213> ORGANISM: unknown  
W--> 129 <220> FEATURE:  
W--> 129 <223> OTHER INFORMATION:  
W--> 129 <400> 8  
131 KRRPVKVYP -9  
135 <210> SEQ ID NO: 9  
137 <211> LENGTH: 12  
E--> 139 <212> TYPE: peptide  
141 <213> ORGANISM: unknown  
W--> 144 <220> FEATURE:  
W--> 144 <223> OTHER INFORMATION:  
W--> 144 <400> 9  
146 PVGKKRRPVK VY -12  
150 <210> SEQ ID NO: 10  
152 <211> LENGTH: 12  
E--> 154 <212> TYPE: peptide  
156 <213> ORGANISM: unknown  
W--> 160 <220> FEATURE:  
W--> 160 <223> OTHER INFORMATION:  
W--> 160 <400> 10  
162 KPVGKKRRPV XV -12  
166 <210> SEQ ID NO: 11  
168 <211> LENGTH: 12

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Input Set : A:\PTO.YF.txt

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E--&gt; 170 &lt;212&gt; TYPE: peptide

172 &lt;213&gt; ORGANISM: unknown

W--&gt; 175 &lt;220&gt; FEATURE:

W--&gt; 175 &lt;223&gt; OTHER INFORMATION:

W--&gt; 175 &lt;400&gt; 11

177 GKPVGKKRRP VK

12

181 &lt;210&gt; SEQ ID NO: 12

183 &lt;211&gt; LENGTH: 13

E--&gt; 185 &lt;212&gt; TYPE: peptide

187 &lt;213&gt; ORGANISM: unknown

W--&gt; 190 &lt;220&gt; FEATURE:

W--&gt; 190 &lt;223&gt; OTHER INFORMATION:

W--&gt; 190 &lt;400&gt; 12

192 TFAGNAVRRS VGO

13

196 &lt;210&gt; SEQ ID NO: 13

198 &lt;211&gt; LENGTH: 6

E--&gt; 200 &lt;212&gt; TYPE: peptide

202 &lt;213&gt; ORGANISM: unknown

W--&gt; 205 &lt;220&gt; FEATURE:

W--&gt; 205 &lt;223&gt; OTHER INFORMATION:

W--&gt; 205 &lt;400&gt; 13

207 PLGLWA

6

211 &lt;210&gt; SEQ ID NO: 14

213 &lt;211&gt; LENGTH: 5

E--&gt; 215 &lt;212&gt; TYPE: peptide

217 &lt;213&gt; ORGANISM: unknown

W--&gt; 220 &lt;220&gt; FEATURE:

W--&gt; 220 &lt;223&gt; OTHER INFORMATION:

W--&gt; 220 &lt;400&gt; 14

222 PLFYS

5

226 &lt;210&gt; SEQ ID NO: 15

228 &lt;211&gt; LENGTH: 5

E--&gt; 230 &lt;212&gt; TYPE: peptide

232 &lt;213&gt; ORGANISM: unknown

W--&gt; 235 &lt;220&gt; FEATURE:

W--&gt; 235 &lt;223&gt; OTHER INFORMATION:

W--&gt; 235 &lt;400&gt; 15

237 PRTLTL

5

241 &lt;210&gt; SEQ ID NO: 16

243 &lt;211&gt; LENGTH: 5

E--&gt; 245 &lt;212&gt; TYPE: peptide

247 &lt;213&gt; ORGANISM: unknown

W--&gt; 250 &lt;220&gt; FEATURE:

W--&gt; 250 &lt;223&gt; OTHER INFORMATION:

W--&gt; 250 &lt;400&gt; 16

252 PLRLS

5

256 &lt;210&gt; SEQ ID NO: 17

258 &lt;211&gt; LENGTH: 6

E--&gt; 260 &lt;212&gt; TYPE: peptide

## RAW SEQUENCE LISTING

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Input Set : A:\PTO.YF.txt

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262 <213> ORGANISM: unknown  
W--> 265 <220> FEATURE:  
W--> 265 <223> OTHER INFORMATION:  
W--> 265 <400> 17  
267 HSSKLO 6  
271 <210> SEQ ID NO: 18  
273 <211> LENGTH: 6  
E--> 275 <212> TYPE: peptide  
277 <213> ORGANISM: unknown  
W--> 280 <220> FEATURE:  
W--> 280 <223> OTHER INFORMATION:  
W--> 280 <400> 18  
282 SQYSNT 6  
286 <210> SEQ ID NO: 19  
288 <211> LENGTH: 7  
E--> 290 <212> TYPE: peptide  
292 <213> ORGANISM: unknown  
W--> 295 <220> FEATURE:  
W--> 295 <223> OTHER INFORMATION:  
W--> 295 <400> 19  
297 QFYSSNK 7  
301 <210> SEQ ID NO: 20  
303 <211> LENGTH: 12  
E--> 305 <212> TYPE: peptide  
307 <213> ORGANISM: unknown  
W--> 310 <220> FEATURE:  
W--> 310 <223> OTHER INFORMATION:  
W--> 310 <400> 20  
312 VSQNYPIVQN FN 12

The types of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

see p. 6 for more  
errors

see sample Sequence Listing  
(attached in back)

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: PCT/US03/27372

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Input Set : A:\PTO.YF.txt  
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*error  
explanation*

Use of <220> Feature (NEW RULES) :

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27

Seq#:28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51

Seq#:52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75

Seq#:76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99

Seq#:100,101,102,103,104,105,106,107,108,109,110,111

Per/4503/27372 6

<210> 111

<211> 50

<212> peptide

<213> unknown

<400> '111

GYKDPPFCVA PLDPQFYSSN KGGGSGGGG SGGGSGYKD PPFCVAPLDP

50

1

delete  
at end of file

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\02022004\PU27372.raw

L:5 M:201 W: Mandatory field data missing, <130> FILE REFERENCE  
L:7 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:19 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:24 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:1, <213>  
ORGANISM:unknown  
L:24 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>  
ORGANISM:unknown  
L:24 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:24  
L:34 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:39 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>  
ORGANISM:unknown  
L:39 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>  
ORGANISM:unknown  
L:39 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:39  
L:49 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:54 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:3, <213>  
ORGANISM:unknown  
L:54 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>  
ORGANISM:unknown  
L:54 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:54  
L:64 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:69 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>  
ORGANISM:unknown  
L:69 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>  
ORGANISM:unknown  
L:69 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:69  
L:79 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:84 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>  
ORGANISM:unknown  
L:84 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>  
ORGANISM:unknown  
L:84 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:84  
L:94 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:99 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>  
ORGANISM:unknown  
L:99 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>  
ORGANISM:unknown  
L:99 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:99  
L:109 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:114 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>  
ORGANISM:unknown  
L:114 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>  
ORGANISM:unknown  
L:114 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:114  
L:124 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:129 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>  
ORGANISM:unknown  
L:129 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>  
ORGANISM:unknown  
L:129 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:129  
L:139 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:144 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:9, <213>  
ORGANISM:unknown

L:144 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>  
ORGANISM:unknown  
L:144 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:144  
L:154 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:160 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>  
ORGANISM:unknown  
L:160 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>  
ORGANISM:unknown  
L:160 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:160  
L:170 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:175 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:11, <213>  
ORGANISM:unknown  
L:175 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>  
ORGANISM:unknown  
L:175 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:175  
L:185 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:190 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:12, <213>  
ORGANISM:unknown



# VERIFICATION SUMMARY

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Input Set : A:\PTO.YF.txt

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L:190 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>  
 ORGANISM:unknown  
 L:190 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:190  
 L:200 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:205 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:13, <213>  
 ORGANISM:unknown  
 L:205 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:13, <213>  
 ORGANISM:unknown  
 L:205 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:205  
 L:215 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:220 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:14, <213>  
 ORGANISM:unknown  
 L:220 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>  
 ORGANISM:unknown  
 L:220 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:220  
 L:230 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:235 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:15, <213>  
 ORGANISM:unknown  
 L:235 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>  
 ORGANISM:unknown  
 L:235 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:235  
 L:245 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:250 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:16, <213>  
 ORGANISM:unknown  
 L:250 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:16, <213>  
 ORGANISM:unknown  
 L:250 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:250  
 L:260 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:265 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:17, <213>  
 ORGANISM:unknown  
 L:265 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>  
 ORGANISM:unknown  
 L:275 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:290 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:305 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:320 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:335 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:350 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:365 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:380 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:395 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:410 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:425 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:440 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:455 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:470 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:485 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:500 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:515 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:530 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:545 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:561 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
 L:576 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

L:591 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:606 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:621 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:636 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:651 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:666 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:681 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

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L:696 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:711 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:726 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:741 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:756 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

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<110> Smith, John; Smithgene Inc.  
 <120> Example of a Sequence Listing  
 <130> 01-00001  
 <140> PCT/EP98/00001  
 <141> 1998-12-31  
 <150> US 08/999,999  
 <151> 1997-10-15  
 <160> <  
 <170> PatentIn version 2.0  
 <210> 1  
 <211> 309  
 <212> DNA  
 <213> Paramecium sp.  
 <220>  
 <221> CDS  
 <222> (279)... (389)  
 <300>  
 <301> Doe, Richard  
 <302> Isolation and Characterization of a Gene Encoding a  
 Protease from Paramecium sp.  
 <303> Journal of Genes  
 <304> 1  
 <305> 4  
 <306> 1-7  
 <307> 1988-06-31  
 <308> 123456  
 <309> 1980-06-31  
 <400>  
 agctgtagtc attcctgtgt cctcttctct ctgggcttct ccccttgcta atcagatctc 60  
 agggagagtg tcttgacctt cctctgcctt tgcagcttca caggcaggca ggcaggcagc 120  
 tcatgtggca attgctggca gtgccacagg ccttccagcc aggcctaggg tgggtccgc 180  
 cgcggcgcgg cggccctctt cgcgtctctt tcgcgctctt ctctcgtctt cctctcgtct 240

Consult this

# Appendix 3, page 2

ggacctgatt aggtgagcag gaggagggggg cagttcagc 296  
Met Val Ser Met Phe Ser  
1 5

tct tct ttc aaa tgg cct gga tct tgt tct bct gtt tgt ttg ttc caa 300  
Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val Cys Leu Phe Gln  
10 15 20

tgt ccc aaa gtc ttc ccc tgt cac tca tca ctg cag ccg aat ctt 389  
Cys Pro Lys Val Leu Pro Cys His Ser Ser Leu Gln Pro Asn Leu  
25 30 35

<210> 2  
<211> 37  
<212> PRT  
<213> Paramecium sp.

<<00> 2  
Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu  
1 5 10 15

Phe Val Cys Leu Phe Gln Cys Pro Lys Val Leu Pro Cys His Ser Ser  
20 25 30

Leu Gln Pro Asn Leu  
35

<210> 3  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.

<400> 3  
Met Val Asn Leu Glu Pro Met His Thr Glu Ile  
1 5 10

<210> 4  
<400> 4  
000

[Annex VIII follows]

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M, when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOS	Count includes total number of SEQ ID NOS	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO: #	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown" molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified



base was used in a sequence

H, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.

in feature

<223>

Other Information

Other relevant information; four lines maximum

<300>

Publication Information

Leave blank after <300>

0

<301>

Authors

Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials

0

<302>

Title

0

<303>

Journal

0

<304>

Volume

0

<305>

Issue

0

<306>

Pages

0

<307>

Date

Journal date on which data published; specify as yyyy-mm-dd, MM-yyyy or Season-yyyy

0

<308>

Database Accession Number

Accession number assigned by database including database name

0

<309>

Database Entry Date

Date of entry in database; specify as yyyy-mm-dd or MM-yyyy

0

<310>

Patent Document Number

Document number; for patent-type citations only. Specify as, for example, US 07/999,999

0

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd
<313>	Relevant Residues	FROM (position) TO (position)
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence

5. Section 1.024 is revised to read as follows:

1.024 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.021(c) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;

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